A2

--The complete sequence of the genome of *S. cerevisiae* is available from the Stanford University Saccharomyces genome worldwide website at stanford.edu/Saccharomyces, and is discussed in Goffeau, A *et al.* (1996) *Science* 274:563-567.--

Please replace paragraph [0064] on page 25 with the following paragraph:

A3

--The strains used in the screening method can vary from a single strain altered in expression of a single target gene to a collection of strains representing a selected set of target gene deletions (e.g., a set of genes involved in a selected signaling pathway or members of a selected protein family (e.g., kinases)). In one embodiment, the method of the invention employs a complete genomic set of genetically tailored yeast strains potentially sensitized or resistant to every possible drug target coded by the yeast genome, with each strain carrying a deletion of a single genetic locus. A fifteen-lab international consortium is currently carrying out production of a collection of tagged heterozygous deletion strains. This collection of bar-coded deletions is available at the Stanford University yeast deletion project worldwide website at stanford.edu/group/yeast_deletion_project/deletions3.html.--

Please replace paragraph [0090] on page 37 with the following paragraph:

A4

--The results are summarized in Table 6. The fold induction of the indicated stress response gene is relative to expression levels in the absence of exposure to the indicated stimuli. Conditions other than tunicamycin were obtained from the world wide website of Incyte at proteome.com/databases/YPD, or from other published data (FK506 data from Marton *et al.* (1998) *Nature Medicine* 4:1293, diauxic shift data from DeRisi, J. *et al.* (1997) *Science* 278:680-686, heat shock data from Roth, F.P. *et al.* (1998) *Nature Biotechnol.* 16:939-945 and MMS data from Jelinsky, S.A. and Sampson, L.D. (1999) *Proc. Natl. Acad. Sci. U S A* 96:1486-1491). Information on various genes and open reading frames were obtained from the Yeast Proteome Database (YPD) (Costanzo, *et al.* (2000) The Yeast Proteome Database (YPD) and *Caenorhabditis elegans* Proteome Database (WormPD): comprehensive resources for the organization and comparison of model organism protein information. Nucleic Acids Research 28(1): 73-76. --